



OIPE

RAW SEQUENCE LISTING

DATE: 03/12/2002

PATENT APPLICATION: US/09/734,672

TIME: 15:19:54

Input Set : A:\GL505502US.txt

Output Set: N:\CRF3\03122002\I734672.raw

**Does Not Comply
Corrected Diskette Needed**

SEQUENCE LISTING

```

3 (1) GENERAL INFORMATION:
5   (i) APPLICANT: Murphy, Patricia D.
6           Allen, Antonette C.
7           Alvares, Christopher P.
8           Critz, Brenda S.
9           Olson, Sheri J.
10          Schelter, Denise B.
11          Zeng, Bin
14   (ii) TITLE OF INVENTION: Coding Sequences of the Human
15                               BRCA1 Gene
17   (iii) NUMBER OF SEQUENCES: 72
19   (iv) CORRESPONDENCE ADDRESS:
20          (A) ADDRESSEE: Morgan Lewis & Bockius LLP
21          (B) STREET: 1111 Pennsylvania Ave., N.W.
22          (C) CITY: Washington
23          (D) STATE: District of Columbia
24          (E) COUNTRY: USA
25          (F) ZIP: 20004
27   (v) COMPUTER READABLE FORM:
28          (A) MEDIUM TYPE: Floppy disk
29          (B) COMPUTER: IBM PC compatible
30          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
31          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
33   (vi) CURRENT APPLICATION DATA:
C--> 34          (A) APPLICATION NUMBER: US/09/734,672
C--> 35          (B) FILING DATE: 03-Dec-2000
37   (vii) PRIOR APPLICATION DATA:
38          (A) APPLICATION NUMBER: US 08/966,436
39          (B) FILING DATE: 07-Nov-97
41          (A) APPLICATION NUMBER: US 08/598,591
42          (B) FILING DATE: 12-Feb-96
44   (viii) ATTORNEY/AGENT INFORMATION:
45          (A) NAME: Michael S. Tuscan
46          (B) REGISTRATION NUMBER: 43,210
47          (C) REFERENCE/DOCKET NUMBER: 44921-5055-02-US
49   (ix) TELECOMMUNICATION INFORMATION:
50          (A) TELEPHONE: 202-739-3000
51          (B) TELEFAX: 202-739-3001

```

ERRORED SEQUENCES

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270 (2) INFORMATION FOR SEQ ID NO: 2:

272 (i) SEQUENCE CHARACTERISTICS:

273 (A) LENGTH: 1863 amino acids.

274 (B) TYPE: amino acid

275 (C) STRANDEDNESS: Not Relevant

W--> 276 (D) TOPOLOGY: Not Relevant

278 (ii) MOLECULE TYPE: protein

280 (vi) ORIGINAL SOURCE:

281 (A) ORGANISM: Homo sapiens

282 (B) STRAIN: BRCA1

284 (viii) POSITION IN GENOME:

285 (A) CHROMOSOME/SEGMENT: 17

286 (B) MAP POSITION: 17q21

290 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

292 Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn
293 1 5 10 15
295 Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys
296 20 25 30
298 Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met
299 35 40 45
301 Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys
302 50 55 60
304 Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser
305 65 70 75 80
307 Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp
308 85 90 95
310 Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn
311 100 105 110
313 Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met
314 115 120 125
316 Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn
317 130 135 140
319 Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly
320 145 150 155 160
322 Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr
323 165 170 175
325 Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn
326 180 185 190
328 Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr
329 195 200 205
331 Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala
332 210 215 220
334 Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln
335 225 230 235 240
337 Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg
338 245 250 255
340 His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu
341 260 265 270
343 Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser

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```

344          275          280          285
346 Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe
347          290          295          300
349 Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg
350          305          310          315          320
352 Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr
353          325          330          335
355 Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu
356          340          345          350
358 Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu
359          355          360          365
361 Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu
362          370          375          380
364 Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp
365          385          390          395          400
367 Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu
368          405          410          415
370 Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu
371          420          425          430
373 Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His
374          435          440          445
376 Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr
377          450          455          460
379 Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn
380          465          470          475          480
382 Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg
383          485          490          495
385 Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Arg Pro Thr Ser Gly Leu
386          500          505          510
388 His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr
389          515          520          525
391 Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln
392          530          535          540
394 Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp
395          545          550          555          560
397 Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys
398          565          570          575
400 Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser
401          580          585          590
402 Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys
403          595          600          605
405 Asn Arg Leu Arg Arg Lys Ser Ser Thr Arg His Ile His Ala Leu Glu
406          610          615          620
408 Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln
409          625          630          635          640
411 Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Lys Tyr Asn
412          645          650          655
414 Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys
415          660          665          670

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```

417  Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr
418          675          680          685
420  Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn
421          690          695          700
423  Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu
424          705          710          715          720
426  Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu
427          725          730          735
429  Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu
430          740          745          750
432  Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser
433          755          760          765
435  Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser
436          770          775          780
438  Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys
439          785          790          795          800
441  Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His
442          805          810          815
444  Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro
445          820          825          830
447  Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu
448          835          840          845
450  Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser
451          850          855          860
453  Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu
454          865          870          875          880
456  Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser
457          885          890          895
458  Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys
459          900          905          910
461  Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly
462          915          920          925
464  Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys
465          930          935          940
467  Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly
468          945          950          955          960
470  Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn
471          965          970          975
473  Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr
474          980          985          990
476  Lys Cys Lys Lys Asn Leu Leu Glu Asn Phe Glu Glu His Ser Met
477          995          1000          1005
479  Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val Ser
480          1010          1015          1020
482  Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly Ala Ser
483          1025          1030          1035          1040
485  Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser
486          1045          1050          1055
488  Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile Gln Ala Glu Leu

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489		1060		1065		1070													
491	Gly	Arg	Asn	Arg	Gly	Pro	Lys	Leu	Asn	Ala	Met	Leu	Arg	Leu	Gly	Val			
492		1075						1080				1085							
494	Leu	Gln	Pro	Glu	Val	Tyr	Lys	Gln	Ser	Leu	Pro	Gly	Ser	Asn	Cys	Lys			
495		1090					1095					1100							
497	His	Pro	Glu	Ile	Lys	Lys	Gln	Glu	Tyr	Glu	Glu	Val	Val	Gln	Thr	Val			
498	1105				1110					1115						1120			
500	Asn	Thr	Asp	Phe	Ser	Pro	Tyr	Leu	Ile	Ser	Asp	Asn	Leu	Glu	Gln	Pro			
501			1125					1130				1135							
503	Met	Gly	Ser	Ser	His	Ala	Ser	Gln	Val	Cys	Ser	Glu	Thr	Pro	Asp	Asp			
504		1140					1145					1150							
506	Leu	Leu	Asp	Asp	Gly	Glu	Ile	Lys	Glu	Asp	Thr	Ser	Phe	Ala	Glu	Asn			
507		1155					1160					1165							
509	Asp	Ile	Lys	Glu	Ser	Ser	Ala	Val	Phe	Ser	Lys	Ser	Val	Gln	Arg	Gly			
510		1170					1175					1180							
512	Glu	Leu	Ser	Arg	Ser	Pro	Ser	Pro	Phe	Thr	His	Thr	His	Leu	Ala	Gln			
513	1185				1190					1195						1200			
514	Gly	Tyr	Arg	Arg	Gly	Ala	Lys	Lys	Leu	Glu	Ser	Ser	Glu	Glu	Asn	Leu			
515			1205					1210				1215							
517	Ser	Ser	Glu	Asp	Glu	Glu	Leu	Pro	Cys	Phe	Gln	His	Leu	Leu	Phe	Gly			
518		1220					1225					1230							
520	Lys	Val	Asn	Asn	Ile	Pro	Ser	Gln	Ser	Thr	Arg	His	Ser	Thr	Val	Ala			
521		1235					1240					1245							
523	Thr	Glu	Cys	Leu	Ser	Lys	Asn	Thr	Glu	Glu	Asn	Leu	Leu	Ser	Leu	Lys			
524		1250					1255					1260							
526	Asn	Ser	Leu	Asn	Asp	Cys	Ser	Asn	Gln	Val	Ile	Leu	Ala	Lys	Ala	Ser			
527	1265				1270					1275						1280			
529	Gln	Glu	His	His	Leu	Ser	Glu	Glu	Thr	Lys	Cys	Ser	Ala	Ser	Leu	Phe			
530		1285						1290				1295							
532	Ser	Ser	Gln	Cys	Ser	Glu	Leu	Glu	Asp	Leu	Thr	Ala	Asn	Thr	Asn	Thr			
533		1300					1305					1310							
535	Gln	Asp	Pro	Phe	Leu	Ile	Gly	Ser	Ser	Lys	Gln	Met	Arg	His	Gln	Ser			
536		1315					1320					1325							
538	Glu	Ser	Gln	Gly	Val	Gly	Leu	Ser	Asp	Lys	Glu	Leu	Val	Ser	Asp	Asp			
539		1330					1335					1340							
541	Glu	Glu	Arg	Gly	Thr	Gly	Leu	Glu	Glu	Asn	Asn	Gln	Glu	Glu	Gln	Ser			
542	1345					1350				1355						1360			
544	Met	Asp	Ser	Asn	Leu	Gly	Glu	Ala	Ala	Ser	Gly	Cys	Glu	Ser	Glu	Thr			
545		1365						1370				1375							
547	Ser	Val	Ser	Glu	Asp	Cys	Ser	Gly	Leu	Ser	Ser	Gln	Ser	Asp	Ile	Leu			
548		1380					1385					1390							
550	Thr	Thr	Gln	Arg	Asp	Thr	Met	Gln	His	Asn	Leu	Ile	Lys	Leu	Gln				
551		1395					1400					1405							
553	Gln	Glu	Met	Ala	Glu	Leu	Glu	Ala	Val	Leu	Glu	Gln	His	Gly	Ser	Gln			
554		1410					1415					1420							
556	Pro	Ser	Asn	Ser	Tyr	Pro	Ser	Ile	Ile	Ser	Asp	Ser	Ser	Ala	Leu	Glu			
557	1425					1430				1435						1440			
559	Asp	Leu	Arg	Asn	Pro	Glu	Gln	Ser	Thr	Ser	Glu	Lys	Ala	Val	Leu	Thr			
560			1445					1450				1455							

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E-->

```

562 Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu
563           1460           1465           1470
565 Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn
566           1475           1480           1485
568 Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu
569           1490           1495           1500
570 Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg
571 1505           1510           1515           1520
573 Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu
574           1525           1530           1535
576 Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr
577           1540           1545           1550
579 Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile
580           1555           1560           1565
582 Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp Pro Ser Glu Asp Arg Ala
583           1570           1575           1580
585 Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu
586 1585           1590           1595           1600
588 Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Gly Pro Ala Ala
589           1605           1610           1615
591 Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val
592           1620           1625           1630
594 Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys
595 1635 1640 1645
597 Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu
598 1650           1655           1660
600 Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile
601 1665           1670           1675           1680
603 Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val
604           1685           1690           1695
606 Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp
607           1700           1705           1710
609 Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met
610 1715           1720           1725
612 Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg
613 1730           1735           1740
615 Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile
616 1745           1750           1755           1760
618 Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro
619           1765           1770           1775
621 Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val
622 1780           1785           1790
624 Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val
625 1795           1800           1805
626 Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile
627 1810           1815           1820
629 Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp
630 1825           1830           1835           1840
632 Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro

```

move Numbering
to the left
1 space

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```

633          1845          1850          1855
635      Gln Ile Pro His Ser His Tyr
636          1860
855 (2) INFORMATION FOR SEQ ID NO: 4:
857      (i) SEQUENCE CHARACTERISTICS:
858          (A) LENGTH: 1863 amino acids
859          (B) TYPE: amino acid
860          (C) STRANDEDNESS: Not Relevant
W--> 861      (D) TOPOLOGY: Not Relevant
863      (ii) MOLECULE TYPE: protein
865      (vi) ORIGINAL SOURCE:
866          (A) ORGANISM: Homo sapiens
867          (B) STRAIN: BRCA1
869      (viii) POSITION IN GENOME:
870          (A) CHROMOSOME/SEGMENT: 17
871          (B) MAP POSITION: 17q21
875      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
877      Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn
878      1          5          10          15
880      Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys
881          20          25          30
883      Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met
884          35          40          45
886      Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys
887          50          55          60
889      Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser
890          65          70          75          80
892      Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp
893          85          90          95
895      Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn
896          100          105          110
898      Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met
899          115          120          125
901      Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn
902          130          135          140
904      Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly
905          145          150          155          160
907      Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr
908          165          170          175
910      Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn
911          180          185          190
913      Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr
914          195          200          205
916      Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala
917          210          215          220
919      Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln
920          225          230          235          240
922      Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg
923          245          250          255

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```

925 His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu
926           260           265           270
928 Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser
929           275           280           285
931 Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe
932           290           295           300
934 Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg
935           305           310           315           320
937 Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr
938           325           330           335
940 Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu
941           340           345           350
943 Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu
944           355           360           365
946 Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu
947           370           375           380
949 Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp
950           385           390           395           400
952 Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu
953           405           410           415
955 Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu
956           420           425           430
958 Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His
959           435           440           445
961 Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr
962           450           455           460
964 Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn
965           465           470           475           480
967 Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg
968           485           490           495
970 Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Arg Pro Thr Ser Gly Leu
971           500           505           510
973 His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr
974           515           520           525
976 Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln
977           530           535           540
979 Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp
980           545           550           555           560
982 Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys
983           565           570           575
985 Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser
986           580           585           590
987 Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys
988           595           600           605
990 Asn Arg Leu Arg Arg Lys Ser Ser Thr Arg His Ile His Ala Leu Glu
991           610           615           620
993 Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln
994           625           630           635           640
996 Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Lys Tyr Asn

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997				645					650				655
999	Gln	Met	Pro	Val	Arg	His	Ser	Arg	Asn	Leu	Gln	Leu	Met
1000				660					665				670
1002	Glu	Pro	Ala	Thr	Gly	Ala	Lys	Lys	Ser	Asn	Lys	Pro	Asn
1003				675					680				685
1005	Ser	Lys	Arg	His	Asp	Ser	Asp	Thr	Phe	Pro	Glu	Leu	Lys
1006				690					695				700
1008	Ala	Pro	Gly	Ser	Phe	Thr	Lys	Cys	Ser	Asn	Thr	Ser	Glu
1009													
1011	Phe	Val	Asn	Pro	Ser	Leu	Pro	Arg	Glu	Glu	Lys	Glu	Glu
1012													
1014	Thr	Val	Lys	Val	Ser	Asn	Asn	Ala	Glu	Asp	Pro	Lys	Asp
1015				740					745				750
1017	Ser	Gly	Glu	Arg	Val	Leu	Gln	Thr	Glu	Arg	Ser	Val	Glu
1018				755					760				765
1020	Ile	Ser	Leu	Val	Pro	Gly	Thr	Asp	Tyr	Gly	Thr	Gln	Glu
1021				770					775				780
1023	Leu	Leu	Glu	Val	Ser	Thr	Leu	Gly	Lys	Ala	Lys	Thr	Glu
1024													
1026	Cys	Val	Ser	Gln	Cys	Ala	Ala	Phe	Glu	Asn	Pro	Lys	Gly
1027													
1029	Gly	Cys	Ser	Lys	Asp	Asn	Arg	Asn	Asp	Thr	Glu	Gly	Phe
1030				820					825				830
1032	Leu	Gly	His	Glu	Val	Asn	His	Ser	Arg	Glu	Thr	Ser	Ile
1033				835					840				845
1035	Glu	Ser	Glu	Leu	Asp	Ala	Gln	Tyr	Leu	Gln	Asn	Thr	Phe
1036				850					855				860
1038	Lys	Arg	Gln	Ser	Phe	Ala	Leu	Phe	Ser	Asn	Pro	Gly	Asn
1039													
1041	Glu	Cys	Ala	Thr	Phe	Ser	Ala	His	Ser	Gly	Ser	Leu	Lys
1042													
1043	Pro	Lys	Val	Thr	Phe	Glu	Cys	Glu	Gln	Lys	Glu	Glu	Asn
1044				900					905				910
1046	Asn	Glu	Ser	Asn	Ile	Lys	Pro	Val	Gln	Thr	Val	Asn	Ile
1047				915					920				925
1049	Phe	Pro	Val	Val	Gly	Gln	Lys	Asp	Lys	Pro	Val	Asp	Asn
1050				930					935				940
1052	Ser	Ile	Lys	Gly	Gly	Ser	Arg	Phe	Cys	Leu	Ser	Ser	Gln
1053				945					950				955
1055	Asn	Glu	Thr	Gly	Leu	Ile	Thr	Pro	Asn	Lys	His	Gly	Leu
1056													
1058	Pro	Tyr	Arg	Ile	Pro	Pro	Leu	Phe	Pro	Ile	Lys	Ser	Phe
1059				980					985				990
1061	Lys	Cys	Lys	Lys	Asn	Leu	Leu	Glu	Glu	Asn	Phe	Glu	Glu
1062				995					1000				1005
1064	Ser	Pro	Glu	Arg	Glu	Met	Gly	Asn	Glu	Asn	Ile	Pro	Ser
1065				1010					1015				1020
1067	Thr	Ile	Ser	Arg	Asn	Asn	Ile	Arg	Glu	Asn	Val	Phe	Lys
1068				1025					1030				1035
													1040

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```

1070 Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser
1071                               1045                               1050                               1055
1073 Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile Gln Ala Glu Leu
1074                               1060                               1065                               1070
1076 Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met Leu Arg Leu Gly Val
1077                               1075                               1080                               1085
1079 Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu Pro Gly Ser Asn Cys Lys
1080                               1090                               1095                               1100
1082 His Pro Glu Ile Lys Lys Gln Glu Tyr Glu Glu Val Val Gln Thr Val
1083                               1105                               1110                               1115                               1120
1085 Asn Thr Asp Phe Ser Pro Tyr Leu Ile Ser Asp Asn Leu Glu Gln Pro
1086                               1125                               1130                               1135
1088 Met Gly Ser Ser His Ala Ser Gln Val Cys Ser Glu Thr Pro Asp Asp
1089                               1140                               1145                               1150
1091 Leu Leu Asp Asp Gly Glu Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn
1092                               1155                               1160                               1165
1094 Asp Ile Lys Glu Ser Ser Ala Val Phe Ser Lys Ser Val Gln Lys Gly
1095                               1170                               1175                               1180
1097 Glu Leu Ser Arg Ser Pro Ser Pro Phe Thr His Thr His Leu Ala Gln
1098                               1185                               1190                               1195                               1200
1099 Gly Tyr Arg Arg Gly Ala Lys Lys Leu Glu Ser Ser Glu Glu Asn Leu
1100                               1205                               1210                               1215
1102 Ser Ser Glu Asp Glu Glu Leu Pro Cys Phe Gln His Leu Leu Phe Gly
1103                               1220                               1225                               1230
1105 Lys Val Asn Asn Ile Pro Ser Gln Ser Thr Arg His Ser Thr Val Ala
1106                               1235                               1240                               1245
1108 Thr Glu Cys Leu Ser Lys Asn Thr Glu Glu Asn Leu Leu Ser Leu Lys
1109                               1250                               1255                               1260
1111 Asn Ser Leu Asn Asp Cys Ser Asn Gln Val Ile Leu Ala Lys Ala Ser
1112                               1265                               1270                               1275                               1280
1114 Gln Glu His His Leu Ser Glu Glu Thr Lys Cys Ser Ala Ser Leu Phe
1115                               1285                               1290                               1295
1117 Ser Ser Gln Cys Ser Glu Leu Glu Asp Leu Thr Ala Asn Thr Asn Thr
1118                               1300                               1305                               1310
1120 Gln Asp Pro Phe Leu Ile Gly Ser Ser Lys Gln Met Arg His Gln Ser
1121                               1315                               1320                               1325
1123 Glu Ser Gln Gly Val Gly Leu Ser Asp Lys Glu Leu Val Ser Asp Asp
1124                               1330                               1335                               1340
1126 Glu Glu Arg Gly Thr Gly Leu Glu Glu Asn Asn Gln Glu Glu Gln Ser
1127                               1345                               1350                               1355                               1360
1129 Met Asp Ser Asn Leu Gly Glu Ala Ala Ser Gly Cys Glu Ser Glu Thr
1130                               1365                               1370                               1375
1132 Ser Val Ser Glu Asp Cys Ser Gly Leu Ser Ser Gln Ser Asp Ile Leu
1133                               1380                               1385                               1390
1135 Thr Thr Gln Gln Arg Asp Thr Met Gln His Asn Leu Ile Lys Leu Gln
1136                               1395                               1400                               1405
1138 Gln Glu Met Ala Glu Leu Glu Ala Val Leu Glu Gln His Gly Ser Gln
1139                               1410                               1415                               1420
1141 Pro Ser Asn Ser Tyr Pro Ser Ile Ile Ser Asp Ser Ser Ala Leu Glu

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1142 1425 1430 1435 1440
 1144 Asp Leu Arg Asn Pro Glu Gln Ser Thr Ser Glu Lys Ala Val Leu Thr
 1145 1445 1450 1455
 1147 Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu
 1148 1460 1465 1470
 1150 Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn
 1151 1475 1480 1485
 1153 Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu
 1154 1490 1495 1500
 1155 Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg
 1156 1505 1510 1515 1520
 1158 Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu
 1159 1525 1530 1535
 1161 Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr
 1162 1540 1545 1550
 1164 Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile
 1165 1555 1560 1565
 1167 Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp Pro Ser Glu Asp Arg Ala
 1168 1570 1575 1580
 1170 Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu
 1171 1585 1590 1595 1600
 1173 Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Ser Pro Ala Ala
 1174 1605 1610 1615
 1176 Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val
 1177 1620 1625 1630
 1179 Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys
 E--> 1180 1635 1640 1645 — move numbering to the left 1 space
 1182 Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu
 1183 1650 1655 1660
 1185 Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile
 1186 1665 1670 1675 1680
 1188 Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val
 1189 1685 1690 1695
 1191 Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp
 1192 1700 1705 1710
 1194 Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met
 1195 1715 1720 1725
 1197 Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg
 1198 1730 1735 1740
 1200 Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile
 1201 1745 1750 1755 1760
 1203 Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro
 1204 1765 1770 1775
 1206 Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val
 1207 1780 1785 1790
 1209 Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val
 1210 1795 1800 1805
 1211 Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile
 1212 1810 1815 1820

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Input Set : A:\GL505502US.txt

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1214 Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp
 1215 1825 1830 1835 1840
 1217 Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro
 1218 1845 1850 1855
 1220 Gln Ile Pro His Ser His Tyr
 1221 1860
 1440 (2) INFORMATION FOR SEQ ID NO: 6:
 1442 (i) SEQUENCE CHARACTERISTICS:
 1443 (A) LENGTH: 1863 amino acids
 1444 (B) TYPE: amino acid
 1445 (C) STRANDEDNESS: Not Relevant
 W--> 1446 (D) TOPOLOGY: Not Relevant
 1448 (ii) MOLECULE TYPE: protein
 1450 (vi) ORIGINAL SOURCE:
 1451 (A) ORGANISM: Homo sapiens
 1452 (B) STRAIN: BRCA1
 1454 (viii) POSITION IN GENOME:
 1455 (A) CHROMOSOME/SEGMENT: 17
 1456 (B) MAP POSITION: 17q21
 1460 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 1462 Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn
 1463 1 5 10 15
 1465 Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys
 1466 20 25 30
 1468 Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met
 1469 35 40 45
 1471 Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys
 1472 50 55 60
 1474 Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser
 1475 65 70 75 80
 1477 Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp
 1478 85 90 95
 1480 Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn
 1481 100 105 110
 1483 Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met
 1484 115 120 125
 1486 Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn
 1487 130 135 140
 1489 Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly
 1490 145 150 155 160
 1492 Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr
 1493 165 170 175
 1495 Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn
 1496 180 185 190
 1498 Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr
 1499 195 200 205
 1501 Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala
 1502 210 215 220
 1504 Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln

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1505	225	230	235	240
1507	Pro Ser Asn Asn Asp	Leu Asn Thr Thr Glu	Lys Arg Ala Ala Glu	Arg
1508		245	250	255
1510	His Pro Glu Lys Tyr	Gln Gly Ser Ser Val	Ser Asn Leu His Val	Glu
1511		260	265	270
1513	Pro Cys Gly Thr Asn	Thr His Ala Ser Ser	Leu Gln His Glu	Asn Ser
1514		275	280	285
1516	Ser Leu Leu Leu Thr	Lys Asp Arg Met Asn	Val Glu Lys Ala	Glu Phe
1517		290	295	300
1519	Cys Asn Lys Ser Lys	Gln Pro Gly Leu Ala	Arg Ser Gln His	Asn Arg
1520		305	310	315
1522	Trp Ala Gly Ser Lys	Glu Thr Cys Asn Asp	Arg Arg Thr Pro	Ser Thr
1523		325	330	335
1525	Glu Lys Lys Val Asp	Leu Asn Ala Asp Pro	Leu Cys Glu Arg	Lys Glu
1526		340	345	350
1528	Trp Asn Lys Gln Lys	Leu Pro Cys Ser Glu	Asn Pro Arg Asp	Thr Glu
1529		355	360	365
1531	Asp Val Pro Trp Ile	Thr Leu Asn Ser Ser	Ile Gln Lys Val	Asn Glu
1532		370	375	380
1534	Trp Phe Ser Arg Ser	Asp Glu Leu Leu Gly	Ser Asp Asp Ser	His Asp
1535		385	390	395
1537	Gly Glu Ser Glu Ser	Asn Ala Lys Val Ala	Asp Val Leu Asp	Val Leu
1538		405	410	415
1540	Asn Glu Val Asp Glu	Tyr Ser Gly Ser Ser	Glu Lys Ile Asp	Leu Leu
1541		420	425	430
1543	Ala Ser Asp Pro His	Glu Ala Leu Ile Cys	Lys Ser Glu Arg	Val His
1544		435	440	445
1546	Ser Lys Ser Val Glu	Ser Asn Ile Glu Asp	Lys Ile Phe Gly	Lys Thr
1547		450	455	460
1549	Tyr Arg Lys Lys Ala	Ser Leu Pro Asn Leu	Ser His Val Thr	Glu Asn
1550		465	470	475
1552	Leu Ile Ile Gly Ala	Phe Val Thr Glu Pro	Gln Ile Ile Gln	Glu Arg
1553		485	490	495
1555	Pro Leu Thr Asn Lys	Leu Lys Arg Lys Arg	Arg Pro Thr Ser	Gly Leu
1556		500	505	510
1558	His Pro Glu Asp Phe	Ile Lys Lys Ala Asp	Leu Ala Val Gln	Lys Thr
1559		515	520	525
1561	Pro Glu Met Ile Asn	Gln Gly Thr Asn Gln	Thr Glu Gln Asn	Gly Gln
1562		530	535	540
1564	Val Met Asn Ile Thr	Asn Ser Gly His Glu	Asn Lys Thr Lys	Gly Asp
1565		545	550	555
1567	Ser Ile Gln Asn Glu	Lys Asn Pro Asn Pro	Ile Glu Ser Leu	Glu Lys
1568		565	570	575
1570	Glu Ser Ala Phe Lys	Thr Lys Ala Glu Pro	Ile Ser Ser Ser	Ile Ser
1571		580	585	590
1572	Asn Met Glu Leu Glu	Leu Asn Ile His Asn	Ser Lys Ala Pro	Lys Lys
1573		595	600	605
1575	Asn Arg Leu Arg Arg	Lys Ser Ser Thr Arg	His Ile His Ala	Leu Glu
1576		610	615	620

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1578	Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln
1579	625 630 635 640
1581	Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Lys Tyr Asn
1582	645 650 655
1584	Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys
1585	660 665 670
1587	Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr
1588	675 680 685
1590	Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn
1591	690 695 700
1593	Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu
1594	705 710 715 720
1596	Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu
1597	725 730 735
1599	Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu
1600	740 745 750
1602	Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser
1603	755 760 765
1605	Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser
1606	770 775 780
1608	Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys
1609	785 790 795 800
1611	Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His
1612	805 810 815
1614	Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro
1615	820 825 830
1617	Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu
1618	835 840 845
1620	Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser
1621	850 855 860
1623	Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu
1624	865 870 875 880
1626	Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser
1627	885 890 895
1628	Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys
1629	900 905 910
1631	Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly
1632	915 920 925
1634	Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys
1635	930 935 940
1637	Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly
1638	945 950 955 960
1640	Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn
1641	965 970 975
1643	Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr
1644	980 985 990
1646	Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met
1647	995 1000 1005
1649	Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val Ser

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Input Set : A:\GL505502US.txt

Output Set: N:\CRF3\03122002\I734672.raw

1650	1010	1015	1020
1652	Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly Ala Ser		
1653	1025	1030	1035
1655	Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser		1040
1656		1045	1050
1658	Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile Gln Ala Glu Leu		1055
1659		1060	1065
1661	Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met Leu Arg Leu Gly Val		1070
1662		1075	1080
1664	Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu Pro Gly Ser Asn Cys Lys		1085
1665	1090	1095	1100
1667	His Pro Glu Ile Lys Lys Gln Glu Tyr Glu Glu Val Val Gln Thr Val		
1668	1105	1110	1115
1670	Asn Thr Asp Phe Ser Pro Tyr Leu Ile Ser Asp Asn Leu Glu Gln Pro		1120
1671		1125	1130
1673	Met Gly Ser Ser His Ala Ser Gln Val Cys Ser Glu Thr Pro Asp Asp		1135
1674		1140	1145
1676	Leu Leu Asp Asp Gly Glu Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn		1150
1677		1155	1160
1679	Asp Ile Lys Glu Ser Ser Ala Val Phe Ser Lys Ser Val Gln Arg Gly		1165
1680	1170	1175	1180
1682	Glu Leu Ser Arg Ser Pro Ser Pro Phe Thr His Thr His Leu Ala Gln		
1683	1185	1190	1195
1684	Gly Tyr Arg Arg Gly Ala Lys Lys Leu Glu Ser Ser Glu Glu Asn Leu		1200
1685		1205	1210
1687	Ser Ser Glu Asp Glu Glu Leu Pro Cys Phe Gln His Leu Leu Phe Gly		1215
1688		1220	1225
1690	Lys Val Asn Asn Ile Pro Ser Gln Ser Thr Arg His Ser Thr Val Ala		1230
1691		1235	1240
1693	Thr Glu Cys Leu Ser Lys Asn Thr Glu Glu Asn Leu Leu Ser Leu Lys		1245
1694	1250	1255	1260
1696	Asn Ser Leu Asn Asp Cys Ser Asn Gln Val Ile Leu Ala Lys Ala Ser		
1697	1265	1270	1275
1699	Gln Glu His His Leu Ser Glu Glu Thr Lys Cys Ser Ala Ser Leu Phe		1280
1700		1285	1290
1702	Ser Ser Gln Cys Ser Glu Leu Glu Asp Leu Thr Ala Asn Thr Asn Thr		1295
1703		1300	1305
1705	Gln Asp Pro Phe Leu Ile Gly Ser Ser Lys Gln Met Arg His Gln Ser		1310
1706		1315	1320
1708	Glu Ser Gln Gly Val Gly Leu Ser Asp Lys Glu Leu Val Ser Asp Asp		1325
1709	1330	1335	1340
1711	Glu Glu Arg Gly Thr Gly Leu Glu Glu Asn Asn Gln Glu Glu Gln Ser		
1712	1345	1350	1355
1714	Met Asp Ser Asn Leu Gly Glu Ala Ala Ser Gly Cys Glu Ser Glu Thr		1360
1715		1365	1370
1717	Ser Val Ser Glu Asp Cys Ser Gly Leu Ser Ser Gln Ser Asp Ile Leu		1375
1718		1380	1385
1720	Thr Thr Gln Gln Arg Asp Thr Met Gln His Asn Leu Ile Lys Leu Gln		1390
1721		1395	1400
			1405

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```

1723   Gln Glu Met Ala Glu Leu Glu Ala Val Leu Glu Gln His Gly Ser Gln
1724       1410               1415               1420
1726   Pro Ser Asn Ser Tyr Pro Ser Ile Ile Ser Asp Ser Ser Ala Leu Glu
1727       1425               1430               1435               1440
1729   Asp Leu Arg Asn Pro Glu Gln Ser Thr Ser Glu Lys Ala Val Leu Thr
1730               1445               1450               1455
1732   Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu
1733               1460               1465               1470
1735   Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn
1736               1475               1480               1485
1738   Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu
1739               1490               1495               1500
1740   Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg
1741       1505               1510               1515               1520
1743   Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu
1744               1525               1530               1535
1746   Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr
1747               1540               1545               1550
1749   Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile
1750               1555               1560               1565
1752   Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp Pro Ser Glu Asp Arg Ala
1753       1570               1575               1580
1755   Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu
1756       1585               1590               1595               1600
1758   Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Gly Pro Ala Ala
1759               1605               1610               1615
1761   Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val
1762               1620               1625               1630
1764       Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys
E--> 1765       1635               1640               1645
1768   Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu
E--> 1769       1650               1655               1660
1771   Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile
E--> 1772       1665               1670               1675               1680
1774   Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val
E--> 1775               1685               1690               1695
1777   Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp
E--> 1778               1700               1705               1710
1780   Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met
E--> 1781       1715               1720               1725
1783   Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg
E--> 1784       1730               1735               1740
1786   Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile
E--> 1787       1745               1750               1755               1760
1789   Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro
E--> 1790               1765               1770               1775
1792   Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val
E--> 1793       1780               1785               1790
1795   Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val

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Input Set : A:\GL505502US.txt

Output Set: N:\CRF3\03122002\I734672.raw

E--> 1796	1795	1800	1805
1797	Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile		
E--> 1798	1810	1815	1820
1800	Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp		
E--> 1801	1825	1830	1835
1803	Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro		1840
E--> 1804	1845	1850	1855
1806	Gln Ile Pro His Ser His Tyr		
E--> 1807	1860		

VERIFICATION SUMMARY

DATE: 03/12/2002

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Input Set : A:\GL505502US.txt

Output Set: N:\CRF3\03122002\I734672.raw

L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:276 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2
L:595 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:861 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:1180 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:1446 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6
L:1765 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6